

SEQUENCE LISTING

<110> Cytos Biotechnology AG

<120> Polypeptides involved in cell-entry of the Adenoviruses of Subtype B

<130> C62115EP

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<170> PatentIn version 3.1

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<212> DNA

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<223> STP-B region

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<222> (301) .. (314)

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Asp	Ala	Cys	Glu	Glu	Pro	Pro	Thr	Phe	Glu	Ala	Met	Glu	Leu	Ile	Gly
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Lys	Pro	Lys	Pro	Tyr	Tyr	Glu	Ile	Gly	Glu	Arg	Val	Asp	Tyr	Lys	Cys
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50		55		60															
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65					70					75					80				
Asp	Arg	Asn	His	Thr	Trp	Leu	Pro	Val	Ser	Asp	Asp	Ala	Cys	Tyr	Arg				
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Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu
305 310 315 320

Glu Gly Ile Leu Asp Ser Leu Asp Val Trp Val Ile Ala Val Ile Val
325 330 335

Ile Ala Ile Val Val Gly Val Ala Val Ile Cys Val Val Pro Tyr Arg
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<210> 3

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<212> PRT

<213> artificial sequence

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<223> polypeptide sequence of the STP-A region, which is inserted before the STP-B region of CD46 in certain splice variants of CD46

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<211> 1110

<212> DNA

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<213> homo sapiens

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<213> homo sapiens

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- 12 -

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<400> 12

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ctggcggcca tgggtgtgct gctgtactcc ttctcgatg cctgtgagga gccaccaaca 120
tttgaagcta tggagctcat tggtaaacca aaacctact atgagattgg tgaacgagta 180
gattataagt gtaaaaaagg atacttctat atacctctc ttgccacca tactatttgt 240
gatcgggaatc atacatggct acctgtctca gatgacgcct gttatagaga aacatgtcca 300
tatatacggg atcctttaa tggccaagca gtccctgcaa atgggactta cgagtttggt 360
tatcagatgc actttatttg taatgagggt tattacttaa ttggtgaaga aattctatat 420
tgtgaactta aaggatcagt agcaatttgg agcggtaagc cccaatatg tgaaaagggt 480
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tttgagtatc ttgatgcagt aacttatagt tgtgacctg cacctggacc agatccattt 600
tcacttattg gagagagcac gatttattgt ggtgacaatt cagtgtggag tcgtgctgct 660
ccagagtgtg aagtgggtcaa atgtcgattt ccagtagtcg aaaatggaaa acagatatca 720
ggatttggaa aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggtttt 780
tacctcgatg gcagcgacac aattgtctgt gacagtaaca gtacttggga tccccagtt 840
ccaaagtgtc ttaaagggtc taggcctact tacaagcctc cagtctcaaa ttatccagga 900
tattcctaaac ctgaggaagg aatacttgac agtttggatg tt 942

- 13 -

<210> 13

<211> 314

<212> PRT

<213> homo sapiens

<400> 13

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
 1 5 10 15

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser
 20 25 30

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly
 35 40 45

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys
 50 55 60

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys
 65 70 75 80

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg
 85 90 95

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro
 100 105 110

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn
 115 120 125

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys
 130 135 140

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val
 145 150 155 160

Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser
 165 170 175

Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp
 180 185 190

Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile
 195 200 205

- 14 -

Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys
 210 215 220

Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser
 225 230 235 240

Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys
 245 250 255

Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser
 260 265 270

Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Gly Pro Arg
 275 280 285

Pro Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro
 290 295 300

Glu Glu Gly Ile Leu Asp Ser Leu Asp Val
 305 310

<210> 14

<211> 945

<212> DNA

<213> homo sapiens

<400> 14

atggagcctc cggcgccgcg cgagtgtccc ttctcttcc	ggcgctttcc tgggttgctt	60
ctggcgcca tgggtgtgct gctgtactcc ttctccgatg	cctgtgagga gccaccaaca	120
tttgaagcta tggagctcat tggtaaacca aaacctact	atgagattgg tgaacgagta	180
gattataagt gtaaaaaagg ataattctat atacctcctc	ttgccacca tactatttgt	240
gatcggaatc atacatggct acctgtctca gatgacgcct	gttatagaga aacatgtcca	300
tatatacggg atcctttaaa tggccaagca gtccctgcaa	atgggactta cgagtttggt	360
tatcagatgc actttatttg taatgagggt tattacttaa	ttggtgaaga aattctatat	420
tgtgaactta aaggatcagt agcaatttgg agcggtaagc	ccccaatatg tgaaaagggt	480
ttgtgtacac cacctccaaa aataaaaaat ggagaacaca	cctttagtga agtagaagta	540
tttgagtatc ttgatgcagt aacttatagt tgtgatcctg	cacctggacc agatccattt	600
tcacttattg gagagagcac gatttattgt ggtgacaatt	cagtgtggag tcgtgctgct	660

- 15 -

```

ccagagtgtgta aagtgggtcaa atgtcgattt ccagtagtgcg aaaatggaaa acagatatca    720
ggatttgga aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggtttt    780
tacctcgatg gcagcgacac aattgtotgt gacagtaaca gtacttggga tccccagtt    840
ccaaagtgtc ttaaagtgtc gacttcttcc actacaaaat ctccagcgtc cagtgcctca    900
ggatatccta aacctgagga aggaatactt gacagtttgg atgtt                    945

```

<210> 15

<211> 315

<212> PRT

<213> homo sapiens

<400> 15

```

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
1          5          10          15

```

```

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser
          20          25          30

```

```

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly
          35          40          45

```

```

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys
50          55          60

```

```

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys
65          70          75          80

```

```

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg
          85          90          95

```

```

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro
          100          105          110

```

```

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn
          115          120          125

```

```

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys
          130          135          140

```

```

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val
          145          150          155          160

```

- 16 -

Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Glu His Thr Phe Ser
165 170 175

Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp
180 185 190

Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile
195 200 205

Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys
210 215 220

Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser
225 230 235 240

Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys
245 250 255

Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser
260 265 270

Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr
275 280 285

Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Tyr Pro Lys
290 295 300

Pro Glu Glu Gly Ile Leu Asp Ser Leu Asp Val
305 310 315

<210> 16

<211> 987

<212> DNA

<213> homo sapiens

<400> 16

atggagcctc ccggccgccg cgagtgtccc tttccttctt ggcgctttcc tgggttgctt 60

ctggcggcca tgggtgttgc tctgtactcc ttctccgatg cctgtgagga gccaccaaca 120

tttgaagcta tggagctcat tggtaaacca aaaccctact atgagattgg tgaacgagta 180

gattataagt gtaaaaaagg atacttctat atacctctc ttgccacca tactatttgt 240

gatcggaatc atacatggct acctgtctca gatgacgcct gttatagaga aacatgtcca 300

tatatacggg atcctttaaa tggccaagca gtccctgcaa atgggactta cgagtttggt 360

- 17 -

```

tattcagatgc actttatttg taatgagggt tattacttaa ttggtgaaga aattctatat 420
tgtgaactta aaggatcagt agcaatttgg agcggtaagc cccaatatg tgaaaagggt 480
ttgtgtacac cacctccaaa aataaaaaat ggaaaacaca cctttagtga agtagaagta 540
tttgagtatc ttgatgcagt aacttatagt tgtgatcctg cacctggacc agatccattt 600
tcacttattg gagagagcac gatttattgt ggtgacaatt cagtgtggag tcgtgctgct 660
ccagagtgtc aagtgggtcaa atgtcgattt ccagtagtgc aaaatggaaa acagatatca 720
ggatttggaa aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggtttt 780
tacctcgatg gcagcgacac aattgtctgt gacagtaaca gtacttggga tccccagtt 840
ccaaagtgtc ttaaagtgtc gacttcttcc actacaaaat ctccagcgtc cagtgcctca 900
ggctctaggc ctacttacaa gcctccagtc tcaaattatc caggatatcc taaacctgag 960
gaaggaatac ttgacagttt gcatgtt 987

```

<210> 17

<211> 329

<212> PRT

<213> homo sapiens

<400> 17

```

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
1           5           10           15

```

```

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser
          20           25           30

```

```

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly
          35           40           45

```

```

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys
          50           55           60

```

```

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys
          65           70           75           80

```

```

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg
          85           90           95

```

```

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro
          100          105          110

```

- 18 -

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn
 115 120 125

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys
 130 135 140

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val
 145 150 155 160

Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser
 165 170 175

Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp
 180 185 190

Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile
 195 200 205

Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys
 210 215 220

Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser
 225 230 235 240

Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys
 245 250 255

Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser
 260 265 270

Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr
 275 280 285

Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg Pro
 290 295 300

Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu
 305 310 315 320

Glu Gly Ile Leu Asp Ser Leu Asp Val
 325

<210> 18

<211> 1671

<212> DNA

- 19 -

<213> artificial sequence

<220>

<223> Construct encoding a fusion polypeptide between the extracellular domain of CD46 at the N-terminus and a human Fc-gamma3 domain at the C-terminus

<400> 18

```

atggagcctc ccggccgccg cgagtgtccc ttcccttctt ggcgctttcc tgggttgctt      60
ctggcggcca tgggtgttgc gctgtaactc ttctccgatg cctgtgagga gccaccaaca      120
tttgaagcta tggagctcat tggtaaacca aaaccctact atgagattgg tgaacgagta      180
gattataagt gtaaaaaagg atacttctat atacctctc ttgccacca tactatttgt      240
gatcggaatc atacatggct acctgtctca gatgacgcct gttatagaga aacatgtcca      300
tatatacggg atccttttaa tggccaagca gtccctgcaa atgggactta cgagtttggt      360
tatcagatgc actttatttg taatgagggt tattacttaa ttggtgaaga aattctatat      420
tgtgaactta aaggatcagt agcaatttgg agcggtaagc cccaatatg tgaaaagggt      480
ttgtgtacac cacctccaaa aataaaaaat ggaaaacaca ctttagtga agtagaagta      540
tttgagtatc ttgatgcagt aacttatagt tgtgatcctg cacctggacc agatccattt      600
tcacttattg gagagagcac gatttattgt ggtgacaatt cagtgtggag tcgtgctgct      660
ccagagtgtg aagtgggtcaa atgtcgattt ccagtagtcg aaaatggaaa acagatatca      720
ggatttgga aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggtttt      780
tacctcgatg gcagcgacac aattgtctgt gacagtaaca gtacttgga tccccagtt      840
ccaaagtgtc ttaaagtgtc gacttcttcc actacaaaat ctccagcgtc cagtgcctca      900
ggtcctaggc ctacttacaa gcctccagtc tcaaattatc caggatatcc taaacctgag      960
gaaggaatac ttgacagttt ggatgttaag cttactcaca catgcccacc gtgcccagca      1020
cctgaagccg agggggcacc gtcagtcttc ctcttcccc caaaacccaa ggacaccctc      1080
atgatctccc ggaccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagacct      1140
gaggtcaagt tcaactggta cgtggacggc gtggagggtc ataatgcaa gacaaagccg      1200
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag      1260
gactggctga atggcaagga gtacaagtgc aaggtctcca acaaagccct ccagcctcc      1320
atcgagaaaa ccatctccaa agccaaaggg cagccccgag aaccacaggt gtacaccctg      1380
ccccatccc gggatgagct gaccaagaac caggtcagcc tgacctgcct ggtcaaaggc      1440
ttctatccca gcgacatcgc cgtggagtgg gagagcaatg ggagccgga gaacaactac      1500
aagaccacgc ctcccgtgtt ggactccgac ggctccttct tcctctacag caagctcacc      1560

```

- 20 -

gtggacaaga gcaggtggca gcaggggaac gtcttctcat gctccgtgat gcatgaggct 1620
 ctgcacaacc actacacgca gaagagcctc tccctgtctc cgggtaaata a 1671

<210> 19

<211> 556

<212> PRT

<213> artificial sequence

<220>

<223> fusion polypeptide between the extracellular domain of CD46 at the N-terminus and a human Fc-gamma3 domain at the C-terminus

<400> 19

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
 1 5 10 15

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser
 20 25 30

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly
 35 40 45

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys
 50 55 60

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys
 65 70 75 80

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg
 85 90 95

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro
 100 105 110

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn
 115 120 125

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys
 130 135 140

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val
 145 150 155 160

Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser

- 21 -

165	170	175
Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp 180 185 190		
Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile 195 200 205		
Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys 210 215 220		
Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser 225 230 235 240		
Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys 245 250 255		
Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser 260 265 270		
Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr 275 280 285		
Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg Pro 290 295 300		
Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu 305 310 315 320		
Glu Gly Ile Leu Asp Ser Leu Asp Val Lys Leu Thr His Thr Cys Pro 325 330 335		
Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe 340 345 350		
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val 355 360 365		
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe 370 375 380		
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro 385 390 395 400		
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr 405 410 415		

- 22 -

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 420 425 430

Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys Ala
 435 440 445

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 450 455 460

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 465 470 475 480

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 485 490 495

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 500 505 510

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 515 520 525

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 530 535 540

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 545 550 555

<210> 20

<211> 1746

<212> DNA

<213> artificial sequence

<220>

<223> Construct encoding a fusion polypeptide between the extracellular domain of CD46 at the N-terminus and the scFv FRP5 against ErbB-2 at the C-terminus

<400> 20

atggagcctc ccggccgccg cgagtgtccc ttctcttctc ggcgctttcc tgggttgctt	60
ctggcggcca tgggtgttgc tctgtactcc ttctccgatg cctgtgagga gccaccaaca	120
tttgaagcta tggagctcat tggtaaacca aaaccctact atgagattgg tgaacgagta	180
gattataagt gtaaaaaagg atacttctat atacctcttc ttgccaccca tactatttgt	240
gatcggaatc atacatggct acctgtctca gatgacgctt gttatagaga aacatgtcca	300

- 23 -

tatatacggg atccttttaa tggccaagca gtccctgcaa atgggactta cgagtttggg 360
 tatcagatgc actttatttg taatgagggg tattacttaa ttggtgaaga aattctatat 420
 tgtgaactta aaggatcagt agcaatttgg agcggtaagc cccaatatg tgaaaagggt 480
 ttgtgtacac cacctccaaa aataaaaaat ggaaaacaca cctttagtga agtagaagta 540
 tttgagtatc ttgatgcagt aacttatagt tgtgatcctg cacctggacc agatccattt 600
 tcacttattg gagagagcac gatttattgt ggtgacaatt cagtgtggag tcgtgctgct 660
 ccagagtgtg aagtgggtcaa atgtcgattt ccagtagtcg aaaatggaaa acagatatca 720
 ggatttggaa aaaaatttta ctacaaagca acagttatgt ttgaatgcga taagggtttt 780
 tacctcgatg gcagcgacac aattgtctgt gacagtaaca gtacttggga tccccagtt 840
 ccaaagtgtc ttaaagtgtc gacttcttcc actacaaaat ctccagcgtc cagtgcctca 900
 ggtcctaggg ctacttacaa gcctccagtc tcaaattatc caggatatcc taaacctgag 960
 gaaggaatac ttgacagttt ggatgttggc ggccgctctc aggtacaact gcagcagttc 1020
 ggacctgaac tgaagaagcc tggagagaca gtcaagatct cctgcaaggc ctctgggtat 1080
 cctttcacia actatggaat gaactgggtg aagcaggctc caggacaggg tttaaagtgg 1140
 atgggctgga ttaacacttc cactggagag tcaacatttg ctgatgactt caagggacgg 1200
 tttgacttct ctttggaac ctctgccaac actgcctatt tgcagatcaa caacctcaa 1260
 agtgaagaca tggctacata tttctgtgca agatgggagg ttaccacgg ctacgttcct 1320
 tactggggcc aaggaccac ggtcacctgt tcctctggcg gtggcggttc tgggtggcgt 1380
 ggctccggcg gtggcggttc tgacatccag ctgaccagtc ctcacaaatt cctgtccact 1440
 tcagtaggag acagggtcag catcacctgc aaggccagtc aggatgtgta taatgctgtt 1500
 gcctggtatc aacagaaacc aggacaatct cctaaacttc tgatttactc ggcacctcc 1560
 cggtaactg gagtcccttc tcgttccact ggcagtggct ctgggccgga tttcacttcc 1620
 accatcagca gtgtgcaggc tgaagacctg gcagtttatt tctgtcagca acattttcgt 1680
 actccattca cgttcgggtc ggggacaaaa ttggagatcg actacaagga tgacgacgac 1740
 aagtag 1746

<210> 21

<211> 581

<212> PRT

<213> artificial sequence

- 24 -

<220>

<223> fusion polypeptide between the extracellular domain of CD46 at the N-terminus and the scFv FRP5 against ErbB-2 at the C-terminus

<400> 21

Met Glu Pro Pro Gly Arg Arg Glu Cys Pro Phe Pro Ser Trp Arg Phe
1 5 10 15

Pro Gly Leu Leu Leu Ala Ala Met Val Leu Leu Leu Tyr Ser Phe Ser
20 25 30

Asp Ala Cys Glu Glu Pro Pro Thr Phe Glu Ala Met Glu Leu Ile Gly
35 40 45

Lys Pro Lys Pro Tyr Tyr Glu Ile Gly Glu Arg Val Asp Tyr Lys Cys
50 55 60

Lys Lys Gly Tyr Phe Tyr Ile Pro Pro Leu Ala Thr His Thr Ile Cys
65 70 75 80

Asp Arg Asn His Thr Trp Leu Pro Val Ser Asp Asp Ala Cys Tyr Arg
85 90 95

Glu Thr Cys Pro Tyr Ile Arg Asp Pro Leu Asn Gly Gln Ala Val Pro
100 105 110

Ala Asn Gly Thr Tyr Glu Phe Gly Tyr Gln Met His Phe Ile Cys Asn
115 120 125

Glu Gly Tyr Tyr Leu Ile Gly Glu Glu Ile Leu Tyr Cys Glu Leu Lys
130 135 140

Gly Ser Val Ala Ile Trp Ser Gly Lys Pro Pro Ile Cys Glu Lys Val
145 150 155 160

Leu Cys Thr Pro Pro Pro Lys Ile Lys Asn Gly Lys His Thr Phe Ser
165 170 175

Glu Val Glu Val Phe Glu Tyr Leu Asp Ala Val Thr Tyr Ser Cys Asp
180 185 190

Pro Ala Pro Gly Pro Asp Pro Phe Ser Leu Ile Gly Glu Ser Thr Ile
195 200 205

Tyr Cys Gly Asp Asn Ser Val Trp Ser Arg Ala Ala Pro Glu Cys Lys
210 215 220

- 25 -

Val Val Lys Cys Arg Phe Pro Val Val Glu Asn Gly Lys Gln Ile Ser
 225 230 235 240

Gly Phe Gly Lys Lys Phe Tyr Tyr Lys Ala Thr Val Met Phe Glu Cys
 245 250 255

Asp Lys Gly Phe Tyr Leu Asp Gly Ser Asp Thr Ile Val Cys Asp Ser
 260 265 270

Asn Ser Thr Trp Asp Pro Pro Val Pro Lys Cys Leu Lys Val Ser Thr
 275 280 285

Ser Ser Thr Thr Lys Ser Pro Ala Ser Ser Ala Ser Gly Pro Arg Pro
 290 295 300

Thr Tyr Lys Pro Pro Val Ser Asn Tyr Pro Gly Tyr Pro Lys Pro Glu
 305 310 315 320

Glu Gly Ile Leu Asp Ser Leu Asp Val Gly Gly Arg Ser Gln Val Gln
 325 330 335

Leu Gln Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu Thr Val Lys
 340 345 350

Ile Ser Cys Lys Ala Ser Gly Tyr Pro Phe Thr Asn Tyr Gly Met Asn
 355 360 365

Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile
 370 375 380

Asn Thr Ser Thr Gly Glu Ser Thr Phe Ala Asp Asp Phe Lys Gly Arg
 385 390 395 400

Phe Asp Phe Ser Leu Glu Thr Ser Ala Asn Thr Ala Tyr Leu Gln Ile
 405 410 415

Asn Asn Leu Lys Ser Glu Asp Met Ala Thr Tyr Phe Cys Ala Arg Trp
 420 425 430

Glu Val Tyr His Gly Tyr Val Pro Tyr Trp Gly Gln Gly Thr Thr Val
 435 440 445

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 450 455 460

Gly Gly Ser Asp Ile Gln Leu Thr Gln Ser His Lys Phe Leu Ser Thr
 465 470 475 480

- 26 -

Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val
485 490 495

Tyr Asn Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
500 505 510

Leu Leu Ile Tyr Ser Ala Ser Ser Arg Tyr Thr Gly Val Pro Ser Arg
515 520 525

Phe Thr Gly Ser Gly Ser Gly Pro Asp Phe Thr Phe Thr Ile Ser Ser
530 535 540

Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln His Phe Arg
545 550 555 560

Thr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Asp Tyr Lys
565 570 575

Asp Asp Asp Asp Lys
580